

1647 13
DB11/20/02
1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/508,997A

DATE: 10/18/2002
TIME: 10:41:41

Input Set : D:\seqlist.txt
Output Set: N:\CRF4\10182002\I508997A.raw

RECEIVED

OCT 25 2002

P.6
TECH CENTER 1600/2900

3 <110> APPLICANT: MIYATA, Toshio
 5 <120> TITLE OF INVENTION: Megsin Protein
 7 <130> FILE REFERENCE: SHIM-004
 9 <140> CURRENT APPLICATION NUMBER: 09/508,997A
 10 <141> CURRENT FILING DATE: 2000-06-27
 12 <150> PRIOR APPLICATION NUMBER: JP 09-275302
 13 <151> PRIOR FILING DATE: 1997-09-22
 15 <160> NUMBER OF SEQ ID NOS: 44
 17 <170> SOFTWARE: PatentIn Ver. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1143
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(1140)
 28 <400> SEQUENCE: 1
 29 atg gcc tcc ctt gct gca gca aat gca gag ttt tgc ttc aac ctg ttc 48
 30 Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe
 31 1 5 10 15
 33 aga gag atg gat gac aat caa gga aat gga aat gtg ttc ttt tcc tct 96
 34 Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser
 35 20 25 30
 37 ctg agc ctc ttc gct gcc ctg gtc cgc ttg ggc gct caa gat 144
 38 Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp
 39 35 40 45
 41 gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca 192
 42 Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser
 43 50 55 60
 45 gga tat gga aac tct tct aat agt cag tca ggg ctc cag tct caa ctg 240
 46 Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu
 47 65 70 75 80
 49 aaa aga gtt ttt tct gat ata aat gca tcc cac aag gat tat gat ctc 288
 50 Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu
 51 85 90 95
 53 agc att gtg aat ggg ctt ttt gct gaa aaa gtg tat ggc ttt cat aag 336
 54 Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys
 55 100 105 110
 57 gac tac att gag tgt gcc gaa aaa tta tac gat gcc aaa gtg gag cga 384
 58 Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg
 59 115 120 125
 61 gtt gac ttt acg aat cat tta gaa gac act aga cgt aat att aat aag 432
 62 Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys

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63	130	135	140	
65	tgg gtt gaa aat gaa aca cat ggc aaa atc aag aac gtg att ggt gaa			480
66	Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu			
67	145	150	155	160
69	ggt ggc ata agc tca tct gct gta atg gtc ctg gtg aat gct gtg tac			528
70	Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr			
71	165	170	175	
73	ttc aaa ggc aag tgg caa tca gcc ttc acc aag agc gaa acc ata aat			576
74	Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn			
75	180	185	190	
77	tgc cat ttc aaa tct ccc aag tgc tct ggg aag gca gtc gcc atg atg			624
78	Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met			
79	195	200	205	
81	cat cag gaa cgg aag ttc aat ttg tct gtt att gag gac cca tca atg			672
82	His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met			
83	210	215	220	
85	aag att ctt gag ctc aga tac aat ggt ggc ata aac atg tac gtt ctg			720
86	Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu			
87	225	230	235	240
89	ctg cct gag aat gac ctc tct gaa att gaa aac aaa ctg acc ttt cag			768
90	Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln			
91	245	250	255	
93	aat cta atg gaa tgg acc aat cca agg cga atg acc tct aag tat gtt			816
94	Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val			
95	260	265	270	
97	gag gta ttt ttt cct cag ttc aag ata gag aag aat tat gaa atg aaa			864
98	Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys			
99	275	280	285	
101	caa tat ttg aga gcc cta ggg ctg aaa gat atc ttt gat gaa tcc aaa			912
102	Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys			
103	290	295	300	
105	gca gat ctc tct ggg att gct tcg ggg ggt cgt ctg tat ata tca agg			960
106	Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg			
107	305	310	315	320
109	atg atg cac aaa tct tac ata gag gtc act gag gag ggc acc gag gct			1008
110	Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala			
111	325	330	335	
113	act gct gcc aca gga agt aat att gta gaa aag caa ctc cct cag tcc			1056
114	Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser			
115	340	345	350	
117	acg ctg ttt aga gct gac cac cca ttc cta ttt gtt atc agg aag gat			1104
118	Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp			
119	355	360	365	
121	gac atc atc tta ttc agt ggc aaa gtt tct tgc cct tga			
122	Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro			
123	370	375	380	
126	<210> SEQ ID NO: 2			
127	<211> LENGTH: 380			
128	<212> TYPE: PRT			

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129 <213> ORGANISM: Homo sapiens
 131 <400> SEQUENCE: 2
 132 Met Ala Ser Leu Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe
 133 1 5 10 15
 135 Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser
 136 20 25 30
 138 Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp
 139 35 40 45
 141 Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser
 142 50 55 60
 144 Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu
 145 65 70 75 80
 147 Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu
 148 85 90 95
 150 Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys
 151 100 105 110
 153 Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg
 154 115 120 125
 156 Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys
 157 130 135 140
 159 Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu
 160 145 150 155 160
 162 Gly Gly Ile Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
 163 165 170 175
 165 Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn
 166 180 185 190
 168 Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met
 169 195 200 205
 171 His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met
 172 210 215 220
 174 Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu
 175 225 230 235 240
 177 Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln
 178 245 250 255
 180 Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val
 181 260 265 270
 183 Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys
 184 275 280 285
 186 Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys
 187 290 295 300
 189 Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg
 190 305 310 315 320
 192 Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala
 193 325 330 335
 195 Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser
 196 340 345 350
 198 Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp
 199 355 360 365
 201 Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro

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Input Set : D:\seqlist.txt
Output Set: N:\CRF4\10182002\I508997A.raw

202	370	375	380														
205	<210> SEQ ID NO: 3																
206	<211> LENGTH: 1229																
207	<212> TYPE: DNA																
208	<213> ORGANISM: Rattus rattus																
210	<220> FEATURE:																
211	<221> NAME/KEY: CDS																
212	<222> LOCATION: (8)..(1147)																
214	<221> NAME/KEY: unsure																
215	<222> LOCATION: (158)..(160), (287)..(289)																
216	<223> OTHER INFORMATION: n is unknown.																
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219	tttcaaa	atg	gcc	tcc	ctt	gct	gca	gca	aat	gca	gaa	ttt	ggc	ttc	gac	49	
220	Met	Ala	Ser	Leu	Ala	Ala	Ala	Asn	Ala	Glu	Phe	Gly	Phe	Asp			
221	1			5					10								
223	tta	tcc	aga	gag	atg	gat	agt	agt	caa	gga	aac	gga	aat	gta	ttc	ttc	97
224	Leu	Phe	Arg	Glu	Met	Asp	Ser	Ser	Gln	Gly	Asn	Gly	Asn	Val	Phe	Phe	
225	15			20					25				30				
227	tct	tcc	ctg	agc	atc	ttc	act	gcc	ctg	agc	cta	atc	cgt	ttg	ggt	gct	145
228	Ser	Ser	Leu	Ser	Ile	Phe	Thr	Ala	Leu	Ser	Leu	Ile	Arg	Leu	Gly	Ala	
229					35					40			45				
W--> 231	cga	ggt	gac	tgt	nnn	cgt	cag	att	gac	aag	gcc	ctg	cac	ttt	atc	tcc	193
W--> 232	Arg	Gly	Asp	Cys	Xaa	Arg	Gln	Ile	Asp	Lys	Ala	Leu	His	Phe	Ile	Ser	
233				50				55				60					
235	cca	tca	aga	caa	ggg	aat	tca	tcg	aac	agt	cag	cta	gga	ctg	caa	tat	241
236	Pro	Ser	Arg	Gln	Gly	Asn	Ser	Ser	Asn	Ser	Gln	Leu	Gly	Leu	Gln	Tyr	
237				65				70				75					
W--> 239	caa	ttg	aaa	aga	gtt	ctt	gct	gac	ata	aac	tca	tct	cat	aag	gat	nnn	289
W--> 240	Gln	Leu	Lys	Arg	Val	Leu	Ala	Asp	Ile	Asn	Ser	Ser	His	Lys	Asp	Xaa	
241				80				85				90					
243	aaa	ctc	agc	att	gcc	aat	gga	gtt	ttt	gca	gag	aaa	gta	ttt	gat	ttt	337
244	Lys	Leu	Ser	Ile	Ala	Asn	Gly	Val	Phe	Ala	Glu	Lys	Val	Phe	Asp	Phe	
245	95				100					105			110				
247	cat	aag	agc	tat	atg	gag	tgt	gct	gaa	aac	tta	tac	aat	gct	aaa	gtg	385
248	His	Lys	Ser	Tyr	Met	Glu	Cys	Ala	Glu	Asn	Leu	Tyr	Asn	Ala	Lys	Val	
249					115					120			125				
251	gaa	aga	gtt	aat	ttt	aca	aat	gat	ata	caa	gaa	acc	aga	ttt	aaa	att	433
252	Glu	Arg	Val	Asp	Phe	Thr	Asn	Asp	Ile	Gln	Glu	Thr	Arg	Phe	Lys	Ile	
253					130					135			140				
255	aat	aaa	tgg	att	gaa	aat	gaa	aca	cat	ggc	aaa	atc	aag	aag	gtg	ttg	481
256	Asn	Lys	Trp	Ile	Glu	Asn	Glu	Thr	His	Gly	Lys	Ile	Lys	Lys	Val	Leu	
257					145					150			155				
259	ggg	gac	agc	agc	ctc	agc	tca	tca	gct	gtc	atg	gtg	cta	gtg	aat	gct	529
260	Gly	Asp	Ser	Ser	Leu	Ser	Ser	Ala	Val	Met	Val	Leu	Val	Asn	Ala		
261	160				165						170						
263	gtt	tac	ttc	aaa	ggc	aag	tgg	aaa	tcg	gcc	ttc	acc	aag	agt	gat	acc	577
264	Val	Tyr	Phe	Lys	Gly	Lys	Trp	Lys	Ser	Ala	Phe	Thr	Lys	Ser	Asp	Thr	
265	175				180					185			190				
267	ctc	agt	tgc	cat	ttc	agg	tct	ccc	agc	ggt	cct	gga	aaa	gca	gtt	aat	625

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268 Leu Ser Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn
 269 195 200 205
 271 atg atg cat caa gaa cgg agg ttc aat ttg tct acc att cag gag cca 673
 272 Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro
 273 210 215 220
 275 cca atg cag att ctt gag cta caa tat cat ggt ggc ata agc atg tac 721
 276 Pro Met Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr
 277 225 230 235
 279 atc atg ttg ccc gag gat gac cta tcc gaa att gaa agc aag ctg agt 769
 280 Ile Met Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser
 281 240 245 250
 283 ttc cag aat cta atg gac tgg aca aat agc agg aag atg aaa tct cag 817
 284 Phe Gln Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln
 285 255 260 265 270
 287 tat gtg aat gtg ttt ctc ccc cag ttc aag ata gag aaa gat tat gaa 865
 288 Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu
 289 275 280 285
 291 atg agg agc cac ttg aaa tct gta ggc ttg gaa gac atc ttt gtt gag 913
 292 Met Arg Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu
 293 290 295 300
 295 tcc agg gct gat ctg tct gga att gcc tct gga ggt cgt ctc tat gta 961
 296 Ser Arg Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val
 297 305 310 315
 299 tca aag cta atg cac aag tcc ctc ata gag gtc tca gaa gaa ggc acc 1009
 300 Ser Lys Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr
 301 320 325 330
 303 gag gca act gct gcc aca gaa agt aac atc gtt gaa aag cta ctt cct 1057
 304 Glu Ala Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro
 305 335 340 345 350
 307 gaa tcc acg gtg ttc aga gct gac cgc ccc ttt ctg ttt gtc att agg 1105
 308 Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg
 309 355 360 365
 311 aag aat ggc atc atc tta ttt act ggc aaa gtc tcg tgt cct 1147
 312 Lys Asn Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro
 313 370 375 380
 315 tgaaattcta tttggtttca catacactaa caggcatgaa gaaacatcat aagtgaatag 1207
 317 aattgttaatt ggaagtacat gg 1229
 320 <210> SEQ ID NO: 4
 321 <211> LENGTH: 380
 322 <212> TYPE: PRT
 323 <213> ORGANISM: Rattus rattus
 325 <220> FEATURE:
 326 <221> NAME/KEY: UNSURE
 327 <222> LOCATION: 51, 94
 328 <223> OTHER INFORMATION: Xaa is unknown.
 330 <400> SEQUENCE: 4
 331 Met Ala Ser Leu Ala Ala Asn Ala Glu Phe Gly Phe Asp Leu Phe
 332 1 5 10 15
 334 Arg Glu Met Asp Ser Ser Gln Gly Asn Val Phe Phe Ser Ser

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/508,997A

DATE: 10/18/2002
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Input Set : D:\seqlist.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:3; Xaa Pos. 51,94
Seq#:4; Xaa Pos. 51,94
Seq#:24; N Pos. 26,29
Seq#:25; N Pos. 3,9,15
Seq#:26; N Pos. 6,9,12,15,18,21